

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Baumgartner, James W.
Farrah, Theresa M.
Foster, Donald C.
Grant, Frank J.
O'Hara, Patrick J.

(ii) TITLE OF INVENTION: Testis-Specific Receptor

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.
(B) STREET: 1201 Eastlake Avenue East
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0. Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Parker, Gary E.
(B) REGISTRATION NUMBER: 31,648
(C) REFERENCE/DOCKET NUMBER: 95-33

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(A) LENGTH: 1289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) NAME/KEY: CDS
(B) LOCATION: 49..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCCCGCCC	GGGAGAGAGG	CAATATCAAG	GTTTTAAATC	TCGGAGAA	ATG	GCT	TTC		57							
						Met	Ala	Phe								
						1										
GTT	TGC	TTG	GCT	ATC	GGA	TGC	TTA	TAT	ACC	TTT	CTG	ATA	AGC	ACA	ACA	105
Val	Cys	Leu	Ala	Ile	Gly	Cys	Leu	Tyr	Thr	Phe	Leu	Ile	Ser	Thr	Thr	
	5					10					15					
TTT	GGC	TGT	ACT	TCA	TCT	TCA	GAC	ACC	GAG	ATA	AAA	GTT	AAC	CCT	CCT	153
Phe	Gly	Cys	Thr	Ser	Ser	Ser	Asp	Thr	Glu	Ile	Lys	Val	Asn	Pro	Pro	
	20					25				30					35	
CAG	GAT	TTT	GAG	ATA	GTG	GAT	CCC	GGA	TAC	TTA	GGT	TAT	CTC	TAT	TTG	201
Gln	Asp	Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Tyr	Leu	
				40					45					50		
CAA	TGG	CAA	CCC	CCA	CTG	TCT	CTG	GAT	CAT	TTT	AAG	GAA	TGC	ACA	GTG	249
Gln	Trp	Gln	Pro	Pro	Leu	Ser	Leu	Asp	His	Phe	Lys	Glu	Cys	Thr	Val	
			55					60					65			
GAA	TAT	GAA	CTA	AAA	TAC	CGA	AAC	ATT	GGT	AGT	GAA	ACA	TGG	AAG	ACC	297
Glu	Tyr	Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Gly	Ser	Glu	Thr	Trp	Lys	Thr	
		70					75					80				
ATC	ATT	ACT	AAG	AAT	CTA	CAT	TAC	AAA	GAT	GGG	TTT	GAT	CTT	AAC	AAG	345
Ile	Ile	Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	
	85					90					95					

GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT	393
Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn	
100 105 110 115	
GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA	441
Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser	
120 125 130	
CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT	489
Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr	
135 140 145	
TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA	537
Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val	
150 155 160	
CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT	585
Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp	
165 170 175	
CAT GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA	633
His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile	
180 185 190 195	
GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT	681
Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr	
200 205 210	
ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT	729
Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr	
215 220 225	
TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT	777
Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr	
230 235 240	
CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC	825
Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser	
245 250 255	
ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG	873
Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu	
260 265 270 275	

ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA 921
 Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu
 280 285 290

ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA 969
 Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val
 295 300 305

GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT 1017
 Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser
 310 315 320

GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA 1065
 Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys
 325 330 335

ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT 1113
 Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val
 340 345 350 355

ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA 1161
 Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys
 360 365 370

ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT CCATATCAAG 1208
 Met Ile Pro Glu Phe Phe Cys Asp Thr
 375 380

AGACATGGTA TTGACTCAAC AGTTTCCAGT CATGGCCAAA TGTTCATAT GAGTCTCAAT 1268

AAAGTGAATT TTTCTTGCGA A 1289

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
1 5 10 15
Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
20 25 30
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45
Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
50 55 60
Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
65 70 75 80
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
85 90 95
Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100 105 110
Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
115 120 125
Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
130 135 140
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
145 150 155 160
Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
165 170 175
Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
180 185 190
Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
195 200 205
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
210 215 220
Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
225 230 235 240

Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335
 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365
 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 10..1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCGCCC	ATG	GCT	TTC	GTT	TGC	TTG	GCT	ATC	GGA	TGC	TTA	TAT	ACC		48	
	Met	Ala	Phe	Val	Cys	Leu	Ala	Ile	Gly	Cys	Leu	Tyr	Thr			
	1				5				10							
TTT	CTG	ATA	AGC	ACA	ACA	TTT	GGC	TGT	ACT	TCA	TCT	TCA	GAC	ACC	GAG	96
Phe	Leu	Ile	Ser	Thr	Thr	Phe	Gly	Cys	Thr	Ser	Ser	Ser	Asp	Thr	Glu	
	15					20					25					
ATA	AAA	GTT	AAC	CCT	CCT	CAG	GAT	TTT	GAG	ATA	GTG	GAT	CCC	GGA	TAC	144
Ile	Lys	Val	Asn	Pro	Pro	Gln	Asp	Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	
	30				35				40					45		
TTA	GGT	TAT	CTC	TAT	TTG	CAA	TGG	CAA	CCC	CCA	CTG	TCT	CTG	GAT	CAT	192
Leu	Gly	Tyr	Leu	Tyr	Leu	Gln	Trp	Gln	Pro	Pro	Leu	Ser	Leu	Asp	His	
				50					55					60		
TTT	AAG	GAA	TAC	ACA	GTG	GAA	TAT	GAA	CTA	AAA	TAC	CGA	AAC	ATT	GGT	240
Phe	Lys	Glu	Tyr	Thr	Val	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Gly	
			65				70					75				
AGT	GAA	ACA	TGG	AAG	ACC	ATC	ATT	ACT	AAG	AAT	CTA	CAT	TAC	AAA	GAT	288
Ser	Glu	Thr	Trp	Lys	Thr	Ile	Ile	Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	
		80					85					90				
GGG	TTT	GAT	CTT	AAC	AAG	GGC	ATT	GAA	GCG	AAG	ATA	CAC	ACG	CTT	TTA	336
Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	Glu	Ala	Lys	Ile	His	Thr	Leu	Leu	
	95					100					105					
CCA	TGG	CAA	TGC	ACA	AAT	GGA	TCA	GAA	GTT	CAA	AGT	TCC	TGG	GCA	GAA	384
Pro	Trp	Gln	Cys	Thr	Asn	Gly	Ser	Glu	Val	Gln	Ser	Ser	Trp	Ala	Glu	
	110				115					120					125	
ACT	ACT	TAT	TGG	ATA	TCA	CCA	CAA	GGA	ATT	CCA	GAA	ACT	AAA	GTT	CAG	432
Thr	Thr	Tyr	Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr	Lys	Val	Gln	
				130				135						140		
GAT	ATG	GAT	TGC	GTA	TAT	TAC	AAT	TGG	CAA	TAT	TTA	CTC	TGT	TCT	TGG	480
Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu	Cys	Ser	Trp	
			145					150					155			
AAA	CCT	GGC	ATA	GGT	GTA	CTT	CTT	GAT	ACC	AAT	TAC	AAC	TTG	TTT	TAC	528
Lys	Pro	Gly	Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn	Leu	Phe	Tyr	
	160					165						170				

TGG TAT GAG GGC TTG GAT CTT GCA TTA CAG TGT GTT GAT TAC ATC AAG	576
Trp Tyr Glu Gly Leu Asp Leu Ala Leu Gln Cys Val Asp Tyr Ile Lys	
175 180 185	
GCT GAT GGA CAA AAT ATA GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA	624
Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser	
190 195 200 205	
GAC TAT AAA GAT TTC TAT ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG	672
Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys	
210 215 220	
CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA	720
Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys	
225 230 235	
CCT TTG CCG CCA GTC TAT CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA	768
Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu	
240 245 250	
ATT AAG CTG AAA TGG GGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT	816
Ile Lys Leu Lys Trp Gly Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys	
255 260 265	
TTT GAT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT	864
Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr	
270 275 280 285	
GCT ACA GTT GAA AAT GAA ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC	912
Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr	
290 295 300	
CGA CAA TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA	960
Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser	
305 310 315	
GAT GAC GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT	1008
Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly	
320 325 330	
GAA GAC CTA TCG AAG AAA ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT	1056
Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly	
335 340 345	

CCTCTAGA 1167

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100 105 110

Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
340 345 350

Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365

Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Trp Ser Xaa Trp Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 11..1126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTTGGAGAA ATG GCT TTC GTC TAC TTG GCT ATC AGA TGC TTA TGT ACC
 Met Ala Phe Val Tyr Leu Ala Ile Arg Cys Leu Cys Thr
 1 5 10

TTT	CTG	ATA	AGC	ACA	ACA	TTC	GGC	TAT	ACT	TCA	ACT	TCA	GAC	ACC	GAG	97
Phe	Leu	Ile	Ser	Thr	Thr	Phe	Gly	Tyr	Thr	Ser	Thr	Ser	Asp	Thr	Glu	
15						20					25					
ATA	AAA	GTT	AAC	CCA	CCT	CAG	GAT	TTT	GAG	ATA	GTG	GAT	CCC	GGA	TAT	145
Ile	Lys	Val	Asn	Pro	Pro	Gln	Asp	Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	
30					35				40						45	
TTA	GGT	TAT	CTC	TAT	TTG	CAA	TGG	CAA	CCC	CCA	CTG	TCT	CTG	GAT	AAT	193
Leu	Gly	Tyr	Leu	Tyr	Leu	Gln	Trp	Gln	Pro	Pro	Leu	Ser	Leu	Asp	Asn	
			50					55						60		
TTT	AAG	GAA	TGC	ACA	GTG	GAA	TAT	GAA	CTA	AAA	TAC	CGA	AAC	ATT	GGT	241
Phe	Lys	Glu	Cys	Thr	Val	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Gly	
			65				70						75			
AGT	GAA	ACA	TGG	ACG	ACC	ATC	ATT	ACT	AAG	AAT	CTA	CAT	TAC	AAA	GAT	289
Ser	Glu	Thr	Trp	Thr	Thr	Ile	Ile	Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	
		80					85					90				
GGG	TTT	GAT	CTT	AAC	AAG	GGC	ATT	GAA	GCG	AAG	ATA	CAC	ACA	CTT	TTA	337
Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	Glu	Ala	Lys	Ile	His	Thr	Leu	Leu	
95						100					105					
CCA	TGG	CAA	TGC	ACA	AAT	GGA	TCA	GAA	GTT	CAA	AGT	TCC	TGG	GCA	GAA	385
Pro	Trp	Gln	Cys	Thr	Asn	Gly	Ser	Glu	Val	Gln	Ser	Ser	Trp	Ala	Glu	
110					115					120					125	
GCT	ACT	TAT	TGG	ATA	TCG	CCA	CAA	GGA	ATT	CCA	GAA	ACT	AAA	GTT	CAG	433
Ala	Thr	Tyr	Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr	Lys	Val	Gln	
				130				135						140		
GAT	ATG	GAT	TGT	GTA	TAT	TAC	AAT	TGG	CAA	TAT	TTA	CTC	TGT	TCT	TGG	481
Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu	Cys	Ser	Trp	
			145					150					155			
AAA	CCT	GGC	ATA	GGT	GTA	CTT	CTT	GAT	ACC	AAT	TAC	AAC	TTG	TTT	TAC	529
Lys	Pro	Gly	Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn	Leu	Phe	Tyr	
		160					165					170				
TGG	TAT	GAG	GGC	TTG	GAT	CGT	GCA	TTA	CAG	TGT	GTT	GAT	TAC	ATC	AAG	577
Trp	Tyr	Glu	Gly	Leu	Asp	Arg	Ala	Leu	Gln	Cys	Val	Asp	Tyr	Ile	Lys	
175						180					185					

GTT GAT GGA CAA AAT ATT GGA TGC AGA TTT CCC TAT TTG GAG TCA TCA Val Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser 190 195 200 205	625
GAC TAT AAA GAT TTC TAC ATT TGT GTT AAT GGA TCA TCA GAA ACC AAG Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Thr Lys 210 215 220	673
CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys 225 230 235	721
CCT TTG CCA CCA GTC TGT CTT ACT TGT ACT CAG GAG AGT TTA TAT GAA Pro Leu Pro Pro Val Cys Leu Thr Cys Thr Gln Glu Ser Leu Tyr Glu 240 245 250	769
ATT AAG CTG AAA TGG AGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT Ile Lys Leu Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys 255 260 265	817
TTT GTT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT Phe Val Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr 270 275 280 285	865
ACC ACA GTT GAA AAT GAA ACG TAC ACC TTG AAA ATA ACA AAT GAA ACC Thr Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Ile Thr Asn Glu Thr 290 295 300	913
CGA CAG TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser 305 310 315	961
GAT GAT GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGT TGG GAA GTT Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Val 320 325 330	1009
GAA GAA CTA TTG AAG AAA ACT TTG CTA CTT TTC TTG TTA CCA TTT GGT Glu Glu Leu Leu Lys Lys Thr Leu Leu Leu Phe Leu Leu Pro Phe Gly 335 340 345	1057
TTC ATA TTA ATA TTA GTT ATA TTT GTA ACC GGT CTG CTT TTG TGT AAG Phe Ile Leu Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Cys Lys 350 355 360 365	1105
AGA GAC AGC TAC CCG AAA ATG	1126

(2) INFORMATION FOR SEQ ID NO:7:

(A) LENGTH: 372 amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Thr Thr Phe Gly Tyr Thr Ser Thr Ser Asp Thr Glu Ile Lys Val
20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp Asn Phe Lys Glu
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
65 70 75 80

Trp Thr Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Ala Thr Tyr
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
145 150 155 160

Tyr Pro Lys Met
370

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG9802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCTTGATAT GGAAAGTCTT CATGTATC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: AP1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: AP2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO:16:

664050 2500000

20

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

34

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG10319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGGGGCTGG AGCTCGGAGA AATGGCTTTC GTT

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG9820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCCCCACTG TCTCTGGATC ATTTT

25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG9806

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACCTTCCCA GCATTGTTA TCACT

25

(2) INFORMATION FOR SEQ ID NO:24:

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG10320

GGGGGGAGAT CTTCAGACAC CGAGATAAAA GTT

33

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGGGGGCTCG AGTTTCTTCG ATAGGTCTTC ACC

33

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG9882

TTACTCTGTT CTGGGAACC TGG

23

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG10082

ACTCTGTTCT TGGAAACCTG G

21

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG10083

AAATGAAACA TACACCTTGA AAAC

24

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG10081

GCATTGTTTA TCACTCCACT C

21

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG9881

TTCAC TT TGC TTCTTACTAC AAA

23

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZG10389

GACTAGCAGA TCTGGGCTCT TTCTTCGATA GGTCTTCAC

39

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: ZG10314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCGTGATTCT CTGGTCGGTG

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: ZG10315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGATTGCTT TGGCGGTGAG

20

5641090 29000000